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JUL 16 2003

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1600

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/873,106C

DATE: 07/10/2003
TIME: 15:30:17

Input Set : A:\1062.1021-004.txt
Output Set: N:\CRF4\07102003\I873106C.raw

4 <110> APPLICANT: Reinherz, Ellis L.
5 Freund, Christian
6 Li, Jing
7 Nishizawa, Kazuhisa
8 Wagner, Gerhard
10 <120> TITLE OF INVENTION: Cloning and Characterization of a CD2
11 Binding Protein (CD2BP2)
14 <130> FILE REFERENCE: 1062.1021-004
16 <140> CURRENT APPLICATION NUMBER: 09/873,106C
17 <141> CURRENT FILING DATE: 2001-06-01
19 <150> PRIOR APPLICATION NUMBER: US 60/111,007
20 <151> PRIOR FILING DATE: 1998-12-04
22 <150> PRIOR APPLICATION NUMBER: US 60/115,647
23 <151> PRIOR FILING DATE: 1999-01-13
25 <150> PRIOR APPLICATION NUMBER: PCT/US99/26993
26 <151> PRIOR FILING DATE: 1999-11-15
28 <160> NUMBER OF SEQ ID NOS: 25
30 <170> SOFTWARE: FastSEQ for Windows Version 4.0
32 <210> SEQ ID NO: 1
33 <211> LENGTH: 1299
34 <212> TYPE: DNA
35 <213> ORGANISM: Homo sapiens
37 <220> FEATURE:
38 <221> NAME/KEY: CDS
39 <222> LOCATION: (121)...(1143)
41 <400> SEQUENCE: 1
42 agtcctcttc cgggtgatgg cggcgggtgc cccggatgt a gccctggcgc aagcatctct 60
43 tctttttcc acctcgcctt ccgcggattc ccagctttag aaacacctct ttgccccgtc 120
44 atg cca aag agg aaa gtg acc ttc caa ggc gtg gga gat gag gag gat 168
45 Met Pro Lys Arg Lys Val Thr Phe Gln Gly Val Gly Asp Glu Glu Asp
46 1 5 10 15
48 gag gat gaa atc att gtc ccc aag aag aag ctg gtg gac cct gtg gct 216
49 Glu Asp Glu Ile Ile Val Pro Lys Lys Leu Val Asp Pro Val Ala
50 20 25 30
52 ggg tca ggg ggt cct ggg agc cgc ttt aaa ggc aaa cac tct ttg gat 264
53 Gly Ser Gly Gly Pro Gly Ser Arg Phe Lys Gly Lys His Ser Leu Asp
54 35 40 45
56 agc gat gag gag gat gat gat gat ggg ggg tcc agc aaa tat gac 312
57 Ser Asp Glu Glu Asp Asp Asp Gly Gly Ser Ser Lys Tyr Asp
58 50 55 60
60 atc ttg gcc tca gag gat gta gaa ggt cag gag gca gcc aca ctc ccc 360
61 Ile Leu Ala Ser Glu Asp Val Glu Gly Gln Glu Ala Ala Thr Leu Pro
62 65 70 75 80

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64	agc	gag	ggg	ggt	ggt	cg	atc	aca	ccc	ttt	aac	ctg	cag	gag	gag	atg	408
65	Ser	Glu	Gly	Gly	Gly	Arg	Ile	Thr	Pro	Phe	Asn	Leu	Gln	Glu	Glu	Met	
66																95	
	85																
68	gag	gaa	ggc	cac	ttt	gat	gcc	gat	ggc	aac	tac	ttc	ctg	aac	cgg	gat	456
69	Glu	Glu	Gly	His	Phe	Asp	Ala	Asp	Gly	Asn	Tyr	Phe	Leu	Asn	Arg	Asp	
70																110	
	100																
72	gct	cag	atc	cga	gac	agc	tgg	ctg	gac	aac	att	gac	tgg	gtg	aag	atc	504
73	Ala	Gln	Ile	Arg	Asp	Ser	Trp	Leu	Asp	Asn	Ile	Asp	Trp	Val	Lys	Ile	
74																125	
	115																
76	cgg	gag	ggg	cca	cct	ggc	cag	cgc	cag	gcc	tca	gac	tcg	gag	gag	gag	552
77	Arg	Glu	Arg	Pro	Pro	Gly	Gln	Arg	Gln	Ala	Ser	Asp	Ser	Glu	Glu	Glu	
78																140	
	130																
80	gac	agc	ttg	ggc	cag	acc	tca	atg	agt	gcc	caa	gcc	ctc	ttg	gag	gga	600
81	Asp	Ser	Leu	Gly	Gln	Thr	Ser	Met	Ser	Ala	Gln	Ala	Leu	Leu	Glu	Gly	
82	145															160	
		150															
84	ctt	ttg	gag	ctc	cta	ttg	cct	aga	gag	aca	gtg	gtc	ggg	gca	ctg	agg	648
85	Leu	Leu	Glu	Leu	Leu	Pro	Arg	Glu	Thr	Val	Ala	Gly	Ala	Leu	Arg		
86																175	
	165																
88	cgt	ctg	ggg	gcc	cga	gga	ggc	aaa	ggg	aga	aag	ggg	cct	ggg	caa		696
89	Arg	Leu	Gly	Ala	Arg	Gly	Gly	Lys	Gly	Arg	Lys	Gly	Pro	Gly	Gln		
90																190	
	180																
92	ccc	agt	tcc	cct	cag	cgc	ctg	gac	cgg	ctc	tcc	ggg	ttg	gcc	gac	cag	744
93	Pro	Ser	Ser	Pro	Gln	Arg	Leu	Asp	Arg	Leu	Ser	Gly	Leu	Ala	Asp	Gln	
94																205	
	195																
96	atg	gtg	gcc	cgg	ggc	aac	ctt	ggt	gtg	tac	cag	gaa	aca	agg	gaa	cgg	792
97	Met	Val	Ala	Arg	Gly	Asn	Leu	Gly	Val	Tyr	Gln	Glu	Thr	Arg	Glu	Arg	
98																220	
	210																
100	ttg	gct	atg	cgt	ttg	ggg	tgt	tgt	cag	acc	cta	gga	ccc	cac			840
101	Leu	Ala	Met	Arg	Leu	Lys	Gly	Leu	Gly	Cys	Gln	Thr	Leu	Gly	Pro	His	
102	225															240	
		230															
104	aat	ccc	aca	ccc	cca	ccc	tcc	ctg	gac	atg	ttc	gct	gag	ttg	gcg		888
105	Asn	Pro	Thr	Pro	Pro	Ser	Leu	Asp	Met	Phe	Ala	Glu	Glu	Leu	Ala		
106																255	
	245																
108	gag	gag	gaa	ctg	gag	acc	cca	acc	cct	acc	cag	aga	gga	gaa	gca	gag	936
109	Glu	Glu	Glu	Leu	Glu	Thr	Pro	Thr	Gln	Arg	Gly	Glu	Ala	Glu			
110																270	
	260																
112	tcg	cgg	gga	gat	ggt	ctg	gtg	gat	gtg	atg	tgg	gaa	tat	aag	tgg	gag	984
113	Ser	Arg	Gly	Asp	Gly	Leu	Val	Asp	Val	Met	Trp	Glu	Tyr	Lys	Trp	Glu	
114																285	
	275																
116	aac	acg	ggg	gat	gcc	gag	ctg	tat	ggg	ccc	ttc	acc	agc	gcc	cag	atg	1032
117	Asn	Thr	Gly	Asp	Ala	Glu	Leu	Tyr	Gly	Pro	Phe	Thr	Ser	Ala	Gln	Met	
118																300	
	290																
120	cag	acc	tgg	gtg	agt	gaa	ggc	tac	ttc	ccg	gac	ggt	gtt	tat	tgc	cgg	1080
121	Gln	Thr	Trp	Val	Ser	Glu	Gly	Tyr	Phe	Pro	Asp	Gly	Val	Tyr	Cys	Arg	
122	305															320	
		310															
124	aag	ctg	gac	ccc	cct	ggt	ggt	cag	ttc	tac	aac	tcc	aaa	cgc	att	gac	1128
125	Lys	Leu	Asp	Pro	Pro	Gly	Gly	Gln	Phe	Tyr	Asn	Ser	Lys	Arg	Ile	Asp	
126																335	
	325																
128	ttt	gac	ctc	tac	acc	tgagcctgct	ggggggccca	tttgggtggc	ccttctttcc								1183

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129 Phe Asp Leu Tyr Thr
 130 340
 132 tggactttgt ggaggaggca ccaagtgtct caggcagcga ggaaattgga ggcattttt 1243
 133 cagtcaattt ccctttccca ataaaagcct tagttgtta aaaaaaaaaa aaaaaa 1299
 135 <210> SEQ ID NO: 2
 136 <211> LENGTH: 341
 137 <212> TYPE: PRT
 138 <213> ORGANISM: Homo sapiens
 140 <400> SEQUENCE: 2
 141 Met Pro Lys Arg Lys Val Thr Phe Gln Gly Val Gly Asp Glu Glu Asp
 142 1 5 10 15
 143 Glu Asp Glu Ile Ile Val Pro Lys Lys Lys Leu Val Asp Pro Val Ala
 144 20 25 30
 145 Gly Ser Gly Gly Pro Gly Ser Arg Phe Lys Gly Lys His Ser Leu Asp
 146 35 40 45
 147 Ser Asp Glu Glu Asp Asp Asp Gly Gly Ser Ser Lys Tyr Asp
 148 50 55 60
 149 Ile Leu Ala Ser Glu Asp Val Glu Gly Gln Glu Ala Ala Thr Leu Pro
 150 65 70 75 80
 151 Ser Glu Gly Gly Arg Ile Thr Pro Phe Asn Leu Gln Glu Glu Met
 152 85 90 95
 153 Glu Glu Gly His Phe Asp Ala Asp Gly Asn Tyr Phe Leu Asn Arg Asp
 154 100 105 110
 155 Ala Gln Ile Arg Asp Ser Trp Leu Asp Asn Ile Asp Trp Val Lys Ile
 156 115 120 125
 157 Arg Glu Arg Pro Pro Gly Gln Arg Gln Ala Ser Asp Ser Glu Glu Glu
 158 130 135 140
 159 Asp Ser Leu Gly Gln Thr Ser Met Ser Ala Gln Ala Leu Leu Glu Gly
 160 145 150 155 160
 161 Leu Leu Glu Leu Leu Pro Arg Glu Thr Val Ala Gly Ala Leu Arg
 162 165 170 175
 163 Arg Leu Gly Ala Arg Gly Gly Lys Gly Arg Lys Gly Pro Gly Gln
 164 180 185 190
 165 Pro Ser Ser Pro Gln Arg Leu Asp Arg Leu Ser Gly Leu Ala Asp Gln
 166 195 200 205
 167 Met Val Ala Arg Gly Asn Leu Gly Val Tyr Gln Glu Thr Arg Glu Arg
 168 210 215 220
 169 Leu Ala Met Arg Leu Lys Gly Leu Gly Cys Gln Thr Leu Gly Pro His
 170 225 230 235 240
 171 Asn Pro Thr Pro Pro Ser Leu Asp Met Phe Ala Glu Glu Leu Ala
 172 245 250 255
 173 Glu Glu Glu Leu Glu Thr Pro Thr Pro Thr Gln Arg Gly Glu Ala Glu
 174 260 265 270
 175 Ser Arg Gly Asp Gly Leu Val Asp Val Met Trp Glu Tyr Lys Trp Glu
 176 275 280 285
 177 Asn Thr Gly Asp Ala Glu Leu Tyr Gly Pro Phe Thr Ser Ala Gln Met
 178 290 295 300
 179 Gln Thr Trp Val Ser Glu Gly Tyr Phe Pro Asp Gly Val Tyr Cys Arg
 180 305 310 315 320

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Input Set : A:\1062.1021-004.txt
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181 Lys Leu Asp Pro Pro Gly Gly Gln Phe Tyr Asn Ser Lys Arg Ile Asp
182 325 330 335
183 Phe Asp Leu Tyr Thr
184 340
187 <210> SEQ ID NO: 3
188 <211> LENGTH: 26
189 <212> TYPE: PRT
190 <213> ORGANISM: Homo sapiens
192 <400> SEQUENCE: 3
193 Gly Asp Ala Glu Leu Tyr Gly Pro Phe Thr Ser Ala Gln Met Gln Thr
194 1 5 10 15
195 Trp Val Ser Glu Gly Tyr Phe Pro Asp Gly
196 20 25
199 <210> SEQ ID NO: 4
200 <211> LENGTH: 27
201 <212> TYPE: PRT
202 <213> ORGANISM: Caenorhabditis elegans
204 <400> SEQUENCE: 4
205 Gly Pro Asp Ser Glu Lys Tyr Gly Pro Tyr Met Ser Lys Asp Met Leu
206 1 5 10 15
207 Phe Trp Leu Gln Ala Gly Tyr Phe Asn Asp Gly
208 20 25
211 <210> SEQ ID NO: 5
212 <211> LENGTH: 27
213 <212> TYPE: PRT
214 <213> ORGANISM: Caenorhabditis elegans
216 <400> SEQUENCE: 5
217 Asp Pro Thr Glu Thr Arg Arg Gly Pro Phe Pro Lys Asp Gln Met Asn
218 1 5 10 15
219 Val Trp Phe Lys Ala Gly Tyr Phe Thr Asp Glu
220 20 25
223 <210> SEQ ID NO: 6
224 <211> LENGTH: 27
225 <212> TYPE: PRT
226 <213> ORGANISM: Caenorhabditis elegans
228 <400> SEQUENCE: 6
229 Asp Asp Arg Gly Thr Val Gln Gly Pro Tyr Gly Ala Ser Thr Val Leu
230 1 5 10 15
231 Asp Trp Tyr Gln Lys Gly Tyr Phe Ser Asp Asn
232 20 25
235 <210> SEQ ID NO: 7
236 <211> LENGTH: 29
237 <212> TYPE: PRT
238 <213> ORGANISM: Saccharomyces cerevisiae
240 <400> SEQUENCE: 7
241 Asp Thr Gln Gly Gln Ile His Gly Pro Phe Thr Thr Gln Met Met Ser
242 1 5 10 15
243 Gln Trp Tyr Ile Gly Gly Leu Glu Tyr Phe Ala Ser Thr
244 20 25

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Input Set : A:\1062.1021-004.txt
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247 <210> SEQ ID NO: 8
248 <211> LENGTH: 27
249 <212> TYPE: PRT
250 <213> ORGANISM: *Saccharomyces cerevisiae*
252 <400> SEQUENCE: 8
253 Asp Ser Asn Gly Asn Ile Gln Gly Pro Phe Gly Thr Asn Asn Met Ser
254 1 5 10 15
255 Gln Trp Tyr Gln Gly Gly Tyr Phe Thr Pro Thr
256 20 25
259 <210> SEQ ID NO: 9
260 <211> LENGTH: 17
261 <212> TYPE: PRT
262 <213> ORGANISM: Artificial Sequence
264 <220> FEATURE:
265 <223> OTHER INFORMATION: Motif in CD2 binding region of CD2BP2
W--> 268 <221> NAME/KEY: VARIANT
269 <222> LOCATION: 1,2,4,5,6,7,9,10,11,12,13,14,15
270 <223> OTHER INFORMATION: Xaa = Any Amino Acid
W--> 272 <221> VARIANT
273 <222> LOCATION: 3
274 <223> OTHER INFORMATION: Xaa can be Tyr or Phe
W--> 276 <221> VARIANT
277 <222> LOCATION: 8
278 <223> OTHER INFORMATION: Xaa can be Met or Val
W--> 280 <400> 9
W--> 281 Gly Pro Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Trp Xaa Xaa Xaa Gly Tyr
282 1 5 10 15
283 Phe
287 <210> SEQ ID NO: 10
288 <211> LENGTH: 6
289 <212> TYPE: PRT
290 <213> ORGANISM: Artificial Sequence
292 <220> FEATURE:
293 <223> OTHER INFORMATION: CD2BP2 binding region
296 <400> SEQUENCE: 10
297 Pro Pro Pro Gly His Arg
298 1 5
301 <210> SEQ ID NO: 11
302 <211> LENGTH: 70
303 <212> TYPE: PRT
304 <213> ORGANISM: *Homo sapiens*
306 <400> SEQUENCE: 11
307 Pro Pro Pro Pro Pro Gly His Arg Ser Gln Ala Pro Ser His Arg Pro
308 1 5 10 15
309 Pro Pro Pro Gly His Arg Val Gln His Gln Pro Gln Lys Arg Pro Pro
310 20 25 30
311 Ala Pro Ser Gly Thr Gln Val His Gln Gln Lys Gly Pro Pro Leu Pro
312 35 40 45
313 Arg Pro Arg Val Gln Pro Lys Pro Pro His Gly Ala Ala Glu Asn Ser

RAW SEQUENCE LISTING ERROR SUMMARY DATE: 07/10/2003
PATENT APPLICATION: US/09/873,106C TIME: 15:30:18

Input Set : A:\1062.1021-004.txt
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:9; Xaa Pos. 3,4,5,6,7,8,9,10,12,13,14

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L: 268 M: 281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L: 272 M: 258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:9
L: 276 M: 258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:9
L: 280 M: 258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:9
L: 281 M: 341 W: (46) "n" or "Xaa" used, for SEQ ID#:9 after pos.:0